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ALIGNMENTS

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RESULT 1
AAR26449
ID AAR2
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AC AAR2
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AC AAR2
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XX PMON
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5-enolpyruvyl-3-shikimate phosphate synthetase; ACC; ethylene;
Pseudomonas chloroaphis 6G5.
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Delaying fruit ripening and senescence in plants - by controlling ethylene@ prodn., pref. by expression of 1-amino:cyclopropane-1-carboxylic acid deaminase.

WPI; 1992-284334/34. N-PSDB; AAQ27201.

Klee HJ,

Kishore GM;

Disclosure; Page 64-66; 110pp; English.

The sequences given in AAR26448 and AAR26449 are encoded by genes which were used in the construction of an expression plasmid pMONI1030 which was used to transform petunia plants. This plasmid contained the genes for chloroplast transit peptide (CTP2) (AAR26448) and the CP4 synthetic 5 enclyvruy1-3 shikimate phosphate synthetase (EPSPS) gene (AAR26449) which is capable of conferring resistance to glyphosate. The plasmid also contained the 1-aminocyclo-propane-1-carboxylic acid (ACC) deaminase gene from Pseudomonas chloroaphis (see also AAQ27199). The transformed plants had ethylene levels reduced to about one half that of the control, untransformed plants. It is expected that such plants will show reduced

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Best Local
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     WPI; 1998-076419/07
N-PSDB; AAV09719.
                                   Klee HJ,
                                                                             26-DEC-1990;
17-DEC-1991;
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XEEXSCOCOCOCXS
                                                                        Example
                                                                                        Production of plants with delayed ripening - using DNA encoding amino:cyclo:propane-1-carboxylic acid deaminase.
                                                                        9; Fig 21; 56pp;
                                                                        English.
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This sequence represents the synthetic CP4 5-enolpyruvyl-3-shikimate phosphate synthase (EPSPS) gene which is capable of conferring resistar to glyphosate and is used in a novel method for producing fruit-bearing plants with delayed ripening. The method involves the expression of a laminocyclopropane-1-carboxylic acid (ACC) deaminase gene in a plant at level sufficient to reduce ethylene production in the fruit erring resistance y fruit-bearing pression of a 1-

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Query Match
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AAE39920 standard; protein; 455 A

18-DEC-2003 (first entry)

Class I EPSPS enzyme related protein.

ARESULT 3
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ARESUES ARESULS AR Unidentified Glyphosate transgenic US2002168680-A1 plant; tr transgenic; 5-enolpyruvylshikimate-3 uvylshikimate-3 phosphate
herbicide; weed control; synthase; enzyme;
EPSPS.

# 14-NOV-2002

16-DEC-1999; 99US-00464099

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28-AUG-1991;
13-SEP-1994;
07-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to glyphosate tolerant 5-enolpyruvylshikimate-3 phosphate synthase (EPSPS) enzymes and nucleic acid molecules encoding such enzymes. The invention is useful for producing genetically transformed plants which are tolerant to a glyphosate herbicide and for selectively controlling weeds in a field containing a crop having planted crop seeds or plants. The present sequence is a protein related to the
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2288; DB 7; ilarity 100.0%; Pred. No. 1.2e-180; Conservative 0; Mismatches 0;
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91US-00749611.
94US-00306063.
97US-00833485.
98US-00137440.
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ADJ79608;

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Cc polymucleotides and ways to reduce transgence silencing in transgenic cc plants. Specifically, it refers to introducing an artificial polymucleotide that is divergent from an endogenous plant gene, but which cencrodes a substantially identical protein. The present invention cc encodes a substantially identical protein. The present invention cc agronomically useful phenotype, such as drought, cold or herbicide cc tolerance, increased yield and disease or insect resistance. In cc particular, it refers to a modified enolpyruyl-3-phosphoshikimate cc synthase (EPSPS) enzyme required for the synthesis of aromatic amino acids, which is resistant to the phytotoxic herbicide glyphosate. Cc Accordingly, these methods and compositions are useful for plant genetic engineering to produce commercially viable transgenic plants with cc agrobacterium tumefaciens strain CP4 EPSPS protein modified to be glyphosate resistant with chloroplast transit peptide, given in an cc exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 455
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                                                             The invention relates to a transgenic plant which shows resistance to a CC herbicide in an amount inhibiting natural 5-enolpyruvylshikimate-3-CC phosphate synthase (EPSPS) activity of the plant and having at least one CC enzymatic activity selected from: (1) EPSPS activity different from CC enzymatic activity of the plant or (2) glyphosate oxidoreductase CC (GOX) activity different from the natural GOX activity of the plant; and CC in which a gene encoding a protein having the following properties: (a) CC combines specifically with a substance participating to the herbicidic CC combines specifically notenaturing activity on a substantially no denaturing activity on a substantially no denaturing activity on a substance to which said CC protein combines specifically; and (c) contains substantially no CC framework region of the variable region of immunoglobulin. The present CC sequence is that of the Petunia hybrida EPSPS gene. (Updated on 11-SEP-2003 CC to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plant; herbicide resistance; EPSPS; GOX; Petunia hybrida; 5-enolpyruvylshikimate-3-phosphate synthase; glyphosate oxidoreductase; protoporphyrinogen IX oxidase; immunoglobulin; Agrobacterium; strain CP4; chloroplast transit peptide.
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                                                                                                                                                                                                                                                                                                                  5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; glyphosate; shikimic acid pathway; phosphoenolpyruvic acid; 3-phosphoshikimic 5-enolpyruvyl-3-phosphoshikimic acid; herbicide; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW34683;
Region
                                                                              Region
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17-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                          synthase (EPSPS) from Agrobacterium sp. strain
                                                                           /label= characteristic_region
/note= "see AAW34691"
173. .177
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/note= "see AAW34692"
200. .204
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99.8%;
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Pred. No. 3.6e-180;
0; Mismatches 1;
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 KAMQAMGARIRKEGDTWIIDGVGNGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFI

MSHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG

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                                                                                                                                                                                             CC enolpyruvylshikimate-3-phosphate synthases (EPSPS). These novel EPSPS CC enolpyruvylshikimate-3-phosphate synthases (EPSPS). These novel EPSPS CC enzymes have little homology with known Class I EPSPS enzymes, and belong CC to a new class, Class II. The present sequence is from Agrobacterium sp. CC which leads to the biosynthesis of aromatic compounds. EPSPS converts CC phosphoenolpyruvic acid (PEP) and 3-phosphoshikimic acid to 5-enolpyruvyl CC -3-phosphoshikimic acid to 5-enolpyruvyl CC would be useful to produce transgenic crops containing glyphosate. It CC would be useful to produce transgenic crops containing glyphosate. It CC would be useful to produce transgenic crops containing glyphosate. CC resistance genes so that glyphosate-containing herbicides can be applied CC selectively kill weeds. The novel EPSPS enzymes exhibit a low Km for CC the plant is made glyphosate, such that when introduced into a plant, CC peptide to target the protein into the chloroplast, which is the site for CC the shikimic acid pathway. In addition, the EPSPS gene is cloned into a CC plant under the control of a promoter such as figwort mosaic virus containing containing virus containing containing containing containing the site for CC containing pathway. In addition, the EPSPS gene is cloned into a containing cont
                                                               Query Match
Best Local Similarity
Matches 454; Conserv
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28-AUG-1991;
13-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of glyphosate-herbicide tolerant plants - using DNA encoding class II 5-enol:pyruvyl:shikimate-3-phosphate synthase enzyme(s).
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                                                                 454; Conservative
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                                                                                     99.7%;
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                                                               Score 2282; DB 2;
Pred. No. 3.6e-180;
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Matches 454
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25-MAR-2003
02-OCT-1997
                                                                                                                                                                                                                                                 AAW24474 shows the sequence of a class II 5-enolpyruvylshikimate-3-phosphate synthase (EBSPS) enzyme. Class II EPSPS enzymes are tolerant to glyphosate herbicides. EPSPS and sequences encoding it are used for the production of herbicide resistant (glyphosate-tolerant) plants such as corn, wheat, rice, barley, soybean, cotton, sugarbeet, oilseed rape, canola, flax, sunflower, potato, tobacco, tomato, alfalfa, poplar, pine, eucalyptus, apple, lettuce, peas, lentils, grape and turf grasses. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated 5-enol:pyruvyl:shikimate-3-phosphate synthase gefor transforming plants to produce plants which are tolerant glyphosate herbicide.
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                                                                                                                                                                                                     Sequence
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28-AUG-1991;
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DB; AAT77313.
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ilarity 99.8%;
Conservative
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(revised)
(first entry)
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91US-00749611
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                                                                                                 Score 2282; DB 2;
Pred. No. 3.6e-180;
0; Mismatches 1;
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28-AUG-1991;
13-SEP-1994;
                                                                                                                                                               Glyphosate useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-enolpyruvylshikimate-3-phosphate synthase; class II EPSPS enzyme; glyphosate herbicide; transformed bacteria; class I EPSPS enzyme; resistance; ihhibition; 5-enolpyruvyl-3-phosphoshikimic acid;
                                                                                              Claim
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                                                                                                                                                               resistant 5-enol:pyruvyl:shikimate-3-phosphate synthase characterisation of the enzyme to determine inhibition (
                                                                                      3; 152pp;
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91US-00749611.
94US-00306063.
                                                                                                                                                                                                                                                                                                    Padgette
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                                                                                                                                                                                                                                                                                                        Kishore GM,
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An isolated 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) has the sequence domains (I), (II), (III) and (IV): -R-X1-H-X2-E- (I), -G-D-K-X3- (II); -S-A-Q-X4-K- (III); and -N-X5-T-R- (IV). Where X1 = G, S, T, C, Y,

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RESULT 10
AABOSOS3
ID AABOSOS
XX
AC AABOS
XX
AC AABOS
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I1-SE
DT 11-SE
DT 10-SE
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DE Agrob
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                                                                                                              5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; glyphosate; transformed bacteria; transgenic plant; herbicide.
                                                                                                                                                                                      11-SEP-2003
10-SEP-2001
                                                                                                                                                                                                                                                             AAE05053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 455 AA;
 20-AUG-1998;
                              19-JUN-2001.
                                                                                      Agrobacterium
                                                                                                                                                         Agrobacterium
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Pred. No. 3.6e-180;
0; Mismatches 1;
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Matches 454
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28-AUG-1991;
13-SEP-1994;
07-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA probe capable of use in a polymerase chain reaction for identifying the presence of a target genomic DNA encoding a 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) enzyme.
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milarity 99.8%;
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RESULT 11 AAE31621

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360 360 300 300 240 240 180 180 120 60

AAE31621

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The invention relates to a method for detecting or quantifying target CC proteins in complex biological samples, which involves analysing peptide CC fragments via mass spectrometry, where detection of a signature peptide CC indicates the presence of the target protein in the sample. The method is CC complex biological samples, e.g. plants, animals or microorganisms, by CC employing mass spectrometry-based techniques. It can also be applied in CC complex biological samples, e.g. plants, animals or microorganisms, by CC employing mass spectrometry-based techniques. It can also be applied in CC diagnostic analyses, such as detection of genetically CC modified organisms for insect or herbicidal resistance, or in the CC diagnosis of phytopathogenic disease or contamination in plants, soil, CC liquids, solids and other samples from environmental sources. It may also be used to monitor for targeted proteins in manufacturing food processes, and in various clinical and diagnostic analyses, such as monitoring CC enclopyruvylshikimate-3-phosphate synthase (BPSPS) used to illustrate the CC method of the invention
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18-APR-2001;
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2001US-0284713P.
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28-AUG-1991;
13-SEP-1994;
07-APR-1997;
                                               The invention relates to glyphosate tolerant 5-enolpyruvylshikimate-3 phosphate synthase (BPSPS) enzymes and nucleic acid molecules encoding such enzymes. The invention is useful for producing genetically transformed plants which are tolerant to a glyphosate herbicide and for selectively controlling weeds in a field containing a crop having plants crop seeds or plants. The present sequence is Agrobacterium sp. strain CP4 class II EPSPS protein
                                                                                                                                                                                                                                                                                                   New 5-enolpyruvylshikimate-3-phosphate synthase DNA sequence useful producing genetically transformed plants, and selectively controlliweeds in a field containing crop having planted crop seeds or plant
Sequence
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(KISH/)
(PADG/)
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Matches 454; Conserv
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The sequence is that of the Class II 5'-enolpyruvylshikimate-3 phosphate synthase enzyme (EPSPS) of Achromobacter sp. strain LBAA It is used to
                                                                                                                         DNA encoding class II 5'-enoly producing plants and bacteria
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                                                                         Disclosure; Fig 5; 148pp; English.
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                                                                                                                                  VADLKVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAEGATVMMGLEELKVKESDRLSA 360
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                                                                                    VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
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VTVDDSNMIATSFPEFMDMMPGLGAKIELS
                                                                                                                   VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
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82.9%; Pred. No. 1.46
tive 32; Mismatches
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447
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RESULT 14
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XX Glysh
KW Glysh
KW S'-en
XX Pseud
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XX 19-M9
XX 19-M9
XX 28-AL
XX 19-Al
XX
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    Barry GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9204449-A
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03-AUG-1992
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                                                                                                                                                                                      31-AUG-1990;
                                                                                                                                                                                                                                                                           28-AUG-1991;
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                                                                                             (MONS ) MONSANTO
    Kishore GM,
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    Padgette
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RESULT 15
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XX AAW34
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                                      5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; glyphosate; shikimic acid pathway; phosphoenolpyruvic acid; 3-phosphoshikimic scid; herbicide; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
    Pseudomonas
                            glyphosate
                                                                                                  Class II EPSP
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17-FEB-1998
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                                                                                                                                                                                              standard;
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    gp;
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    strain PG2982
                                                                                                                                                                                              protein;
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                            gene; glyphosate-tolerance; promoter
                                                                                                                                                                                               449
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Pred. No. 1.4e-148;
                                                                                             from Pseudomonas sp. strain
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GDASLTKRPMGRVLNPLREMGVQVKSEDGDRLPVTLRGPKTPTPITYRVPMASAQVKSAV

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KAMQAMGARIRKEGDTWIIDGVGNGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFI

RAMQAMGAKIRKEGDVWIINGVGNGCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI

MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG

MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG

Similarity

83.1%; 82.9%;

Conservative

32;

Score 1900.5; Pred. No. 1.4e 32; Mismatches

1.4e-148;

Indels Length

Gaps

60

ВB 2

449; ω --

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CC enzymes have little homology with known Class I EPSPS enzymes, and belong Ct to a new class, Class II. The present sequence was isolated from CC Pseudomonas sp. strain PG2982. The EPSPS enzymes are part of the shikimic CC acid pathway, which leads to the biosynthesis of aromatic compounds. CC EPSPS converts phosphoenolpyruvic acid (PEP) and 3-phosphoshikimic acid cto 5-enolpyruvyl-3-phosphoshikimic acid, and is inhibited by the CC christide glyphosate. It would be useful to produce transgenic crops CC containing glyphosate resistance genes so that glyphosate-containing CC enzymes exhibit a low Km for PEP and a high Ki for glyphosate, such that CC when introduced into a plant, the plant is made glyphosate-tolerant, and CE PSPS enzyme activity is not affected. These class II EPSPS enzymes are fused to a chloroplast transit peptide to target the protein into the CC chloroplast, which is the site for the shikimic acid pathway. In CC addition, the EPSPS gene is cloned into a plant under the control of a cromoter such as figwort mosaic virus promoter or the cauliflower mosaic corresponded to the control of a chloroplast. So that expression is enhanced. (Updated on 17-OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-1990;
28-AUG-1991;
13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
Sequence
                                                                                                                                                                                                                                                                                                                      AAW34683-89 represent a new class of glyphosate-tolerant enolpyruvylshikimate-3-phosphate synthases (EPSPS). These
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Production of glyphosate-herbicide tolerant plants - using DNA class II 5-enol:pyruvyl:shikimate-3-phosphate synthase enzyme(s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stallings WC,
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                                 to standardise OS
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DB; AAT93790.
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91US-00749611.
94US-00306063.
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'note= "see AAW34693"
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'note= "see AAW34690"
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VIVDDSNMIATSFPEFMDMMPGLGAKIELS 447	421 VTVDDATMIATSFPEFMDLMAGLGAKIELS 450	361 VARGLEANGVDCTEGEMSLTVRGRPDGKGLGGGTVATHLDHRIAMSFLVMGLAAEKP 417	VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP 420	301 VADLKVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA 360	301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAEGATVMNGLEELRVKESDRLSA 360	VPGDPSSTAFPLVAALLVEGSDVTIRNVLMVPTRTGLILTLQEMGADIEVLNARLAGGED 300	241 VPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGED 300	181 LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRHIRITGQGKLVGQTID 240	181 LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID 240	:

Search completed: April 20, 2005, 15:23:13 Job time : 78 secs

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Result
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2288
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Q8yeg1
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coxiella bu
prochlorocc
streptococc
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bradyrhizob
caulobacter
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181 LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID 240

	8 Q	g Q	B &	Query Ma Best Loo Matches	RESULT Q71LY8 OF COC SECOND OF	45	36 37 39 41 42 43
	121 G 121 G	61 K	1 1 3—3	atch cal s	OSS	802.	<b>ထ ထထ ထ ထ ထ ထ</b>
	DASLTKRPM         DASLTKRPM	AMQAMGARI         AMQAMGARI	MLHGASSRPATARKS	imilarity ; Conservat	Y8  PRELIMINARY; PRT; Y8; UL-2004 (TrEMBLrel. 27, Created) UL-2004 (TrEMBLrel. 27, Last sec UL-2004 (TrEMBLrel. 27, Last sec UL-2004 (TrEMBLrel. 27, Last anr PSPS.  ine max (Soybean). ryota; Viridiplantae; Streptoph) ryota; Viridiplantae; Streptoph) ryota; Magnoliophyta; eudico sids I; Fabales; Fabaceae; Papil _TaxID=3847;  ENCE FROM N.A. DY. Lee SI.; CEC-2001) to the EMEL/Ger CATALYTIC ACTIVITY: Phosphoenol; phosphate + 5-O-(1-carboxyviny).) PATHWAY: Aromatic amino acids bi sixth step. SIMILARITY: Belongs to the EPSP SIMILARITY: Be		
	GRVLNPI        GRVLNPI	RKEGDTW        RKEGDTW	TARKSSC         TARKSSC	100. 100.	NARY rel. rel. rel. rel. rel. rel. rel. rel.		423 1 428 1 429 2 428 2 429 2 430 2 430 1 443 1
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	DASLTKRPMGRVLNPLREMGVQVKSEDGDRLPVTLRGPKTPTP 	KAMQAMGARIRKEGDTWIIDGVGNGGLLAPEAPLDFGNAATGCR	SGLSGTVRIPGDKSISHRSFMFGGLASGE 	Score 2288; DB 2; Len Pred. No. 7.8e-129; ; Mismatches 0; Ind	puence update) notation update) tta; Embryophyta tta; Embryophyta tta; Embryophyta tyledons; core ionoideae; Phas yruvate + 3-pho 3-phosphoshiki osynthesis; shi synthase family 1-carboxyvinyl ty; IEA. d family biosyn ino acid biosyn 18307E4AD2C3 CRC	A_LACLC ALIGNMENTS	THETN TISIN ESTRMU  39 313 T3
	PKTPTPITYRVPMASAQVKSA 	FGNAATGCRLTMGLVGVYDFDSTF 	FMFGGLASGETRITGLLEGEDVINTG	Length 455; Indels 0; Gaps	Tracheophyta; ddicots; rosids; leae; Glycine. es. hoshikimate = te. mate pathway; nesis, sh; nesis;	P43905 lactococ	
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Q9R4E4;
30-MAY-2000
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     PROSITE; PS00104; EPSP SYNTHASE 1; 1.

PROSITE; PS00885; EPSP SYNTHASE 2; 1.

Aromatic amino acid biosynthesis; Direct protein Genetically modified food; Herbicide resistance; CONFLICT 2 S-> L (in Ref. 2).

SEQUENCE 455 AA; 47588 MW; 236580D08D6EF422 C
                                                                                                                                                                 HAMAP; MF_00210; -; 1.
InterPro; IPR006264; AroA.
InterPro; IPR001986; EPSP_synth.
Pfam; PF00275; EPSP_synthase; 1.
ProDom; PD001867; EPSP_synth; 1.
TIGRFAMS; TIGR01356; aroA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The expressed protein in glyphosate-tolerant soybean, enolpyruvylshikimate-3-phosphate synthase from Agrobact strain CP4, is rapidly digested in vitro and is not to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=aroA;
Agrobacterium sp. (strain CP4).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bacteria; Proteobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gavaged mice.";
J. Nutr. 126:728-740(1996).
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NCBI_TaxID=361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fuchs R.L., Padgette S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harrison L.A., Bailey M.R., Naylor
Nida D.L., Burnette B.L., Nickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-28; 47-61 AND 321-333. Barry G.F., Kishore G.M., Padgette S.R., Stallings W.C.; "Glyphosate-tolerant 5-enolpyruyJshikimate-3-phosphate synt Patent number US5633435, 27-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96182485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-15.
                                                                                                                                                                                                                                                                                                      SIMECELLULAR LOCATION: Cytoplasmic (Probable).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
BIOTECHNOLOGY: Introduced by genetic manipulation and glyphosate-tolerant soybean, canola, cotton and maize Developed to provide new weed-control options for farm Expression of this protein in plants imparts high leve glyphosate tolerance.
SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate. PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
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iley M.R., Naylor M.W., Ream J.E., Hammond B.G.,
te B.L., Nickson T.E., Mitsky T.A., Taylor M.L.,
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C Q92S\(\text{V}\)5;

IT 28-FEB-2003 (Rel. 41, Last sequence update)

IT 28-FEB-2003 (Rel. 44, Last sequence update)

IT 28-FEB-2003 (Rel. 44, Last annotation update)

IT 05-JUL-2004 (Rel. 44, Last annotation update)

DE 9-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-DE enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)

Name-aroa; OrderedLocusNames=R002S3; ORFNames=SMC00333;

GN Name-aroa; OrderedLocusNames=R002S3; ORFNames=SMC00333;

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
RESULT 3
AROA R
AROA R
AROA R
AC 0925V5
DT 28-FBB
DT 28-FBB
DT 3-phos
DS 6-0-19V1
GN Name-a
OS Rhizob
OC -!- SU
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Best Local Similarity
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                                                                                                        MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
"Analysis of the chromosome sequence of the legume symbiont
sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001)
-i- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate pathway;
                                                                                                                                                                                                                                                                                                                                         STRAIN=1021;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                      sixth step.
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                    SIMILARITY: Belongs to the EPSP synthase family.
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   SWISS-PROT
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Matches 412
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R HAMAP, MF 00210; -; 1.

R INTERPRO; IPR006264; AroA.

R InterPro; IPR001986; EPSP synth.

R Pfam; PF00275; EPSP synthase; 1.

R Pfam; PF00275; EPSP synthase; 1.

R PF0Dom; PD001867; EPSP synth; 1.

R PROSITE; PS00104; EPSP SYNTHASE 1; 1.

R PROSITE; PS00104; EPSP SYNTHASE 2; 1.

R PROSITE; PS00885; EPSP—SYNTHASE 2; 1.

R PROSITE; PS00885; EPSP—SYNTHASE 2; 1.

R PROSITE; PS00885; EPSP—SYNTHASE 2; 1.

SEQUENCE 455 AA; 47900 MW; 97659E1C7E1021B5 CRC64;
                                                                                                AROA PSES2 STANDARD; PRT; 449 AA. P56952; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 05-JUL-2004 imate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP Name=aroA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.,
Barry G.F., Kishore
                                                          Pseudomonas sp. (strain Po
Achromobacter sp. (strain
Bacteria; Proteobacteria.
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                                        NCBI_TaxID=308,
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ilarity 90.5%;
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G.M., Padgett
 Padgette S.R.,
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Pred. No. 1.8e
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  Stallings W.C.;
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- I SUBUNIT: Monomer (By Similarity).

- I SUBUNIT: Monomer (By Similarity).

- I SIMILARITY: Monomer (By Similarity).

- I SIMILARITY: Belongs to the antibiotic glyphosate.

- I SIMILARITY: Belongs to the EPSP synthase family.

R HAMAP; MF 00210; -; 1.

R InterPro; IPR001986; EPSP_synth.

R InterPro; IPR001986; EPSP_synth.

R Pfam; PF00275; EPSP synthase; 1.

R Pfam; PF00275; EPSP synthase; 1.

R ProDom; PD001867; EPSP synthase; 1.

R ProDom; PD001867; EPSP Synthase; 1.

R PROSITE; PS00104; EPSP SYNTHASE_1; 1.

PROSITE; PS00104; EPSP SYNTHASE_1; 1.

APROSITE; PS00185; EPSP SYNTHASE_2; 1.

APROSITE; PS00185; EPSP SYNTHASE_1; 1.

PROSITE; PS00185; EPSP SYNTHASE_1; 1.
                                                             AROA BRUSU STANDARD; PRT; 450 AA. 0863C4; 0963C4; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 3-phosphoshikimate 1-carboxyvinyltransferase enolpyruvylshikimate-3-phosphate synthase) (El Name-aroa; OrderedLocusNames=BR0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicide resistance; Transferase.
SEQUENCE 449 AA; 47297 MW; 447
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- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.

-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthases.";
Patent number US5633435, 27-MAY-1997
 Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                     Bacteria; Proteobacteria;
                                                        Brucella suis.
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82.9%;
                                       Alphaproteobacteria; Rhizobiales;
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Pred. No. 1.1e-105;
2; Mismatches 42;
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synthase)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006264; AroA.
InterPro; IPR006264; AroA.
InterPro; IPR001986; EPSP synth.
Pfam; PF00275; EPSP synthse; 1.
ProDom; PD001867; EPSP synth; 1.
TIGRFAMs; TIGR01356; AroA; 1.
PROSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS001865; EPSP SYNTHASE 1; 1.
PROSITE; PS00885; EPSP SYNTHASE 2; 1.
Aromatic amino acid biosynthesis; Complete proteome; Tigromatic amino acid biosynthesis; Tigromatic
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TIGR; BR0025; -.
HAMAP; MF_00210; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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SEQUENCE FROM
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SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the EPSP synthase family.
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VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
                                                                                                                                                                                                                                                                                                                           LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
                                                                          VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
                                                                                                               LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRHIRIVGQGKLTGQTID
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Biovar 1;
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Pred. No. 1.5e-
33; Mismatches
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es 42;
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STRAIN=16M / ATCC 23456 / Biotype 1;

PubMed=11756688; DOI=10.1073/pnas.221575398;

PubMed=11756688; DOI=10.1073/pnas.221575398;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., L

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsm

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsm

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.

"The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase
enolpyruvylshikimate-3-phosphate synthase) (E
Name=aroA; OrderedLocusNames=BMEI1917;
                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR01356; aToA; 1.

PROSITE; PS00104; EPSP_SYNTHASE 1; 1.

PROSITE; PS00885; EPSP_SYNTHASE 2; 1.

Aromatic amino acid biosynthesis; Complete prote SEQUENCE 450 AA; 47207 MW; 931C4B483C162CB7
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InterPro; IPR006264; AroA.
InterPro; IPR001986; EPSP synth.
Pfam; PF00275; EPSP synthase; 1.
ProDom; PD001867; EPSP synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the EPSP synthase family.
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                                                                                                             {\tt MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG}
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                                                                                                                                                                                                                     Score 1874.5; DB
Pred. No. 4e-104;
4; Mismatches 4
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HAMAP; MF_00210; -; 1.

InterPro; IPR006264; ArOA.

InterPro; IPR006264; ArOA.

InterPro; IPR001986; BSPP_synth.

Pfam; PF00275; EPSP_synthase; 1.

PRODOM; PD001867; EPSP_synth; 1.

TIGRFAM4; TIGR01136; arOA; 1.

TIGRFAM4; TIGR01136; AROA; 1.

PROSITE; PS00104; EPSP_SYNTHASE_1; 1.

PROSITE; PS00104; EPSP_SYNTHASE_1; 1.

PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AROA_BRUAB STANDARD; PRT; 450 AA.

(9)AGV2;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP)
                                                                                                                                                                                     the European Bioinformatics Institute. Then use by non-profit institutions as long modified and this statement is not removed, entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              construction of an aroA mutant.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                       EMBL; AF326475; AAK27445.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brucella abortus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brucellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the aroA gene of Brucella abortus construction of an aroA mutant.":
                                                                                                                                                                                                                                                                                                               sixth step.
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the EPSP synthase family.
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                   There are no restrictions ng as its content is in ved. Usage by and for conved.
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RP SEQUEN
RC STRAIN
RX MEDLIN
RA Kaneko
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RA Watanek
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Best Local S
Matches 364
                                                                                                                                                         MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=1214968;
MEDLINE-21082930; PubMed=11214968;
MEANTAME T., Kato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacte
Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
DNA Res. 7:331-338(2000)
-i- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate
phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate
-i- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase
enolpyruvylshikimate-3-phosphate synthase) (E)
Name=aroA; OrderedLocusNames=mll5213;
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Phyllobacteriaceae; Mesorhizobium.
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                                                   SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                             SUBUNIT: Mo:
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81.4%; Pro
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5.5e-103;
1es 45;
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synthase)
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., Kimura T.,
                                                                                                                                                                                                                                                                                                         symbiotic bacterium
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(EPSPS).
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R HAMAP; MF 00210; -; 1.

RINTEPTC; IPR001986; EPSP_synth.

R InterPrc; IPR001986; EPSP_synth.

R Pfam; PF00275; EPSP synthase; 1.

R Pfam; PF00275; EPSP synth; 1.

R PFCDOm; PD001867; EPSP_Synth; 1.

R PFCDIT; PS0011356; arcA; 1.

R PROSITE; PS001104; EPSP_SYNTHASE 1; 1.

R PROSITE; PS001104; EPSP_SYNTHASE 2; 1.

R PROSITE; PS00185; EPSP_SYNTHASE 2; 1.

R PROSITE; PS00185; EPSP_SYNTHASE 2; 1.

SEQUENCE 452 AA; 47455 MW; 2B52983E3523B938 CRC64;
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Best Local
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                                                                                                                                                                                                                           Q6G0X3 PRELIMINARY; PRT; 442 AA.
Q6G0X3;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
3-phosphoshkimate 1-carboxyvinyltransferase.
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STRAIN=Toulouse;
PubMed=15210978; DOI=10.1073/pnas.0305659101
                                                                                               Bartonellaceae;
NCBI_TaxID=803;
                                                                                                                                                      Bartonella quintana (Rochalimaea
Bacteria, Proteobacteria, Alphap
                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                        Name=aroA; OrderedLocusNames=BQ00880;
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77.8%;
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Pred. No. 1
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c: -i-SIMILARITY: Belongs to the EPSP synthase family.

EMBL; BX897700; CAF25595.1; -.

R G0; G0:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferas. . .;

R G0; G0:0016740; F:transferase activity; IEA.

G0; G0:0016780; F:transferase activity; IEA.

G0; G0:0016089; P:aromatic amino acid family biosynthesis, sh. . .;

R InterPro; IPR006264; AroA Ctransf.

R InterPro; IPR001986; EPSP_synth.

Pfam; PF00275; EPSP synthase; 1.

PFAm; PF00275; EPSP synthase; 1.

PR PTODOM; PD001867; EPSP_synth; 1.

R PTGRFAMs; TIGR01356; aroA; 1.

R PROSITE; PS00104; EPSP_SYNTHASE 1; 1.

Amino-acid biosynthesis; Aromatīc amino acid biosynthesis;

CCmplete proteome; Transferase.

S0 SEQUENCE 442 AA; 47538 MW; 225F15BCFDF6DBBA CRC64;
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Best Local :
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Q6G545
Q6G545;
Q6G545;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
S-phosphoshikimate 1-carboxyvinyltransferase.
Name-aroA; OrderedLocusNames=BH00950;
Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M. La Scola B., Holmberg M., Andersson S.G.E.;

"The louse-borne human pathogen Bartonella quintana is a genomic derivative of the zoonotic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721 (2004).

-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.

-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
                                                                                                                                                                        10
                                                                                                                                                                                                                           423
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Rhizobiales;

SQ OCKW

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RESULT 11
Q6NDP4
ID Q6NDP
AC Q6NDP
DT 05-JU
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Best Local (
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Q6NDP4;
05-JUL-2004
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-i- CARALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
-i- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
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PROSITE; PS00104; EPSP_SYNTHASE 1; 1.

Amino-acid biosynthesis; Aromatic amino
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Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A.,
Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A.,
La Scola B., Holmberg M., Andersson S.G.E.;
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                                                  PRELIMINARY;
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67.0%;
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Pred. No. 1.6e
52; Mismatches
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Matches 263
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PROSITE; PS00885; EPSP SYNTHASE 2; 1.

Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Complete proteome; Transferase.
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STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
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InterPro; IPR001986; EPSP_synth.
Pfam; PF00275; EPSP_synthase; 1.
ProDom; PD001867; EPSP_synth; 1.
TIGRPAMs; TIGR01356; aroA; 1.
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SIMILARITY: Belongs to the EPSP synthase family.

[L; BX572593; CAB25505.1; -.

GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferas.

[GO:0016740; F:transferase activity; IEA.

[GO:0016740; P:aromatic amino acid family biosynthesis, sh.

[GO:0016089; P:aromatic amino acid family biosynthesis, sh.
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                          DATMIATSFPEFMDLMAGLGAK
                                                                                                                   LKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENPVTVD
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                                                                          GGVVATHMDHR I AMSALAMGLASDKPVTVD
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10-OCT-2003 (Rel. 4
10-OCT-2003 (Rel. 4
05-JUL-2004 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006264; AroA.
InterPro; IPR001986; EPSP_synth.
Pfam; PF00275; EPSP_synthase; 1.
ProDom; PD001867; EPSP_synth; 1.
PROSITE; PS00104; EPSP_SYNTHASE 1; 1.
PROSITE; PS00885; EPSP_SYNTHASE 2; 1.
Aromatic amino acid biosynthesis; Complete proteome; Transferase.
Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SEQUENCE 469 AA; 48980 MW; DA55AA4F23BB85D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commons entitles remnires a licentary is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradyrhizobium japonicum.
Brateria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP Name=aroA; OrderedLocusNames=blr0738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRAJA
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SUBUNIT: Monomer (By similarity)
SUBCELLULAR LOCATION: Cytoplasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate. PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the EPSP synthase family.
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                                                                                                                                                                                                                                                                                                                                                                               AVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQV
                                                                                                                                                              DGDASLRSRPMRRILDPLEKMGARVVSGGEGGRLPLTLQGARDPLPITYKTPVASAQIKS
                                                                                                                                                                                       IGDASLTKRPMGRVLNPLREMGVQVKS-EDGDRLPVTLRGPKTPTPITYRVPMASAQVKS
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42, Last sequence up
44, Last annotation
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Pred. No. 1.8e.
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(See http://www.isb-sib.ch/announce/
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STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.I.

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El)

Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,

Frager C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate.
phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway
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28-FEB-2003 (Rel. 41, Last sequence update)
28-CTB-2004 (Rel. 45, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase
enolpyruvylshikimate-3-phosphate synthase) (E
                                                                                                                                                                                                                                                                                                EMBL; AE006017; AAK25551.1; PIR; C87694; C87694.
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL
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ID Q9HZZ6
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                                            RP SEQUENCE FROM N.A.

RC STRAIN=ANCC 15692 / PAO1;

RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Waxrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

"PRT opportunistic pathogen.";

RA Nature 406:959-964(2000).

"RT Opportunistic ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate pathway;

"CC 1- PATHAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Q9HZ69;
01-MAR-2001
01-MAR-2001
01-OCT-2003
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OrderedLocusNames=PA3164;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
still frameshift 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
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amino acid biosynthesis; Complete proteome;
443 AA; 46075 MW; 45E8A1463E10B6EC CRC6
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Belongs to the
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Pred. No. 6.4e-60;
     EPSP
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Q88MOS ID Q88MOS AC Q8 AC Q8 DT 01 DT 01 DE P1 DE P1 DE C3 CN P2 OC P2 OX NO

Bacteria; Proteobacteria; Gamm Pseudomonadaceae; Pseudomonas. Pseudomonas putida (strain

Proteobacteria; Gammaproteobacteria;

Pseudomonadales;

KT2440)

O88M05 PRELIMINARY; PRT; 746 AA.

Q88M05;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Prephenate dehydrogenase, putative/3-phosphoshikimate
carboxyvinyltransferase.
OrderedLocusNames=PP1770;

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Best Local Similarity
Matches 214; Conserv
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GO; GO:0003866; F:3-phosphoshikimate 1-cc
GG; GO:0004665; F:prephenate dehydrogena;
GO; GO:0016740; F:transferase activity;
GO; GO:0016740; F:transferase activity;
GO; GO:0016693; P:aromatic amino acid far
GO; GO:0006571; P:tyrosine biosynthesis;
InterPro; IPR0012664; AroA_Ctransf.
InterPro; IPR001286; EPSP synth.
InterPro; IPR001298; PSP synth.
InterPro; IPR001299; Prephen_dehydrog.
Pfam; PF00275; EPSP synthase; 1.
Pfam; PF002153; PDH; 1.
PTGRFAM6; TIGR01366; BPSP SYNTHASE 1; 1.
PROSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS001885; EPSP_SYNTHASE 2; 1.
Amino-acid biosynthesis; Aromatic amino in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004740; AAG06552.1; PIR; E83250; E83250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p; Q9S400; IRF4.
GG:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferas.
GG:0003665; F:prephenate dehydrogenase (NADP+) activity; II
GG:0016740; F:transferase activity; IEA.
GO:0016089; P:aromatic amino acid family biosynthesis, sh.
GO:0006571; P:tyrosine biosynthesis; IEA.
725
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                                                                                                               NRVAKPLREMGAVIETGPEGRPPMTIRGGQRLTGMHYDMPMASAQVKSCLLLAGLYAAGE
                                                                                                                                                                                                                                                                                                        GRVLNPLREMGVQVKSEDGDRLPVTLRGPKTPTPITYRVPMASAQVKSAVLLAGLNTPGI
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                                                                                                                                                                                                                                                                                                                                                                                                                              ARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIR
                           TSFPEFMDLMAGLGAKIELSD
                                                                            DCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENPVTVDDATMIA
                                                                                                                                                                                    PLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSST
                                                                                                                                                                                                                                TSVTEPAPTRDHTERMLRGFGYPVVVEGS----TAKVESGHKLSATHIEVPADISSAAF
                                                                                                                                                                                                                                                  TTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAF
TSFPNFLALCAQTGIRVAVEN
                                                       KAEPTPDGIVIEG---
                                                                                                                                                                        FLVAASIAEGSELVLOHVGINPTRVGVIEILRLMGGDLSLENOREVGGEPVADIRVRSAR
                                                                                                                                                                                                                                                                                                                                                                             -KEGDTWIIDGVGNGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDASLTKRPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.2%; Score 989.5;
48.5%; Pred. No. 5.9
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                                                         -GAFGGGEVWAHGDHRIAMSFSVASLRASGPIRIHDCANVA
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                            451
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
MEDLINE=22423060; PubMed=12534463;
Meinel C., Paulsen I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferas...
GO; GO:000465; F:prephenate dehydrogenase (NADP+) activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001689; P:aromatic amino acid family biosynthesis, sh...
GO; GO:0006571; P:tyrosine biosynthesis; IEA.
InterPro; IPR006264; AroA_Ctransf.
InterPro; IPR001986; BrSP_synth.
InterPro; IPR001986; BrSP_synth.
InterPro; IPR001986; BrSP_synth.
InterPro; IPR001986; BrSP_synth.
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-!- SIMILARITY: Belongs to the EPSP synthase family.
EMBL; ABO16780; AAN67390.1; -.
HSSP; Q9S400; 1RF4.
TIGR; PP1770; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).

Environ. ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.

-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD001867; EPSP_synth; 1.
TIGRENMS; TIGR01356; aroA; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00275; EPSP_synthase; Pfam; PF02153; PDH; 1.
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      669
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746 AA;
                                                GVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENPVTVDDATM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIR
      GIKCEPTPDGIIDG-----
                                                                                                                   STLKGVTVPEDRAPSMIDEYPILAVAAAFAEGATVMNGLEELRVKESDRLSAVANGLKLN
                                                                                                                                                                                                                                          AFFLVAASIAEGSELVLEHVGINPTRTGVIDILRLMGGDITLENQREVGGEPVADLRVRG
                                                                                                                                                                                                                                                                                                                                                                                                                              GITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSST 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EGPNHGRVTIHGVGLHGLKPPPGPLYVGNSGTSMRLLSGLLAGQPFDVTMTGDASLSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEGDTW----IIDGVGNGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDASLTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQPGGRINGRIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATLQAFRDMGVVI- 374
                                                                                                                                                                                                                                                                                                    AFPLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
                                                                                                                                                                                                                                                                                                                                                                    GKTTVTEPAPTRDHTERMLRGFGYSV----DSHG-PVASLQSGGKLTATRIEVPADISSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMNRVANPLREMGAVVETGPDGRPPLTIRGGHKLKGLTYTLPMASAQVKSCLLLAGLYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMGRVLNPLREMGVQVKSEDGDRLPVTLRGPKTPTPITYRVPMASAQVKSAVLLAGLNTP 188
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Pred. No. 8e-
-GOMGGGEVHGHGDHRIAMAFSVASLRASAPIRIHDCAN
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Search completed: April 20, Job time: 75 secs 2005, 15:25:50

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Database
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Maximum Match 100%
Listing first 45 summaries
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2288
1 MLHGASSRPATARKSSGLSG.....FMDLMAGLGAKIELSDTKAA 455
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Copyright (c) 1993 - 2005 Compugen Ltd.
                  / cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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1087.976 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

13 13 13 13 13 13 13 13	Result No.
2288 2288 2288 2282 2282 2271 1900.5 1900.5 1908.5 1908.5 1855.5 1855.5	Score
100.0 100.0 99.7 99.3 99.3 99.3 83.1 83.1 83.1 83.1 83.1 77.9 53.9	Query
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US-09-861-696-70 US-09-464-099A-70 US-09-464-099A-3 US-09-464-099A-3 US-10-424-599-169346 US-09-861-696-5 US-09-861-696-7 US-09-464-099A-5 US-09-464-099A-7 US-09-464-099A-7 US-10-369-493-12116 US-10-369-493-1216 US-10-369-493-10476	ID
Sequence 70, Appl Sequence 70, Appl Sequence 3, Appli Sequence 3, Appli Sequence 169346, Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 30, Appli Sequence 30, Appli Sequence 12116, A Sequence 1216, A Sequence 10476, A	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	. 32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
521.5	577	577	695	766.5	785	785	785	787	803.5	803.5	806	806	806	806.5		835.5	867.5	867.5	867.5	878	884	906.5	906.5	908.5	908.5	912.5	927.5	983	1135	1149.5	1188.5
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US-10-335-977-6495	US-09-464-099A-44	US-09-861-696-44	-369-493-	10-369-493-113	US-10-369-493-23174	US-09-464-099A-42	US-09-861-696-42	US-10-369-493-8970	US-10-472-928-2780	US-10-369-493-16494	US-10-214-766-31	US-09-464-099A-69	US-09-861-696-69	US-10-369-493-18482	US-10-369-493-9745	US-10-369-493-20917	US-10-369-493-2764	US-09-464-099A-67	US-09-861-696-67	US-10-369-493-13934	US-10-369-493-17242	9	US-10-369-493-15751	US-10-369-493-9499	US-10-369-493-9302	US-10-369-493-17730	0-369-493	US-10-369-493-9974	US-10-369-493-17074	US-10-369-493-18039	US-10-369-493-7814
Sequence 6495, Ap			Sequence 2931, Ap		2317	Sequence 42, Appl	42,	8970,	Sequence 2780, Ap		e 31,	69,	Sequence 69, Appl	18482,	9745,	Sequence 20917, A	Sequence 2764, Ap		O)	13934,	17242,	Sequence 16135, A	15751,	9499,	Sequence 9302, Ap	Sequence 17730, A	15383,	Sequence 9974, Ap	17074,	Sequence 18039, A	Sequence 7814, Ap

## ALIGNMENTS

RESULT 1 US-09-861-696-70 Sequence 7 Patent No.

APPLICANT: Barry, Gerard F.

INFORMATION:

70, Application US/09861696 . US20020007053A1

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PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR FILING DATE: 1997-04-07
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR FILING DATE: 1994-09-13
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR FILING DATE: 1991-08-28
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR FILING DATE: 1990-08-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 70
                                                                                                                              ; TYPE: PRT; ORGANISM: Artificial sequence; FEATURE: ; OTHER INFORMATION: Synthetic US-09-861-696-70
Query Match 100.0%; Score 2288; DB 9; Best Local Similarity 100.0%; Pred. No. 7.4e-182; Matches 455; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUYYLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR PILING DATE: 1998-08-20
PRIOR FILING DATE: 1998-08-20
PRIOR FILING DATE: 1998-08-20
                                                                                                                                                                                                                                                                                                  LENGTH: 455
                                                                Length 455;
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Indels

<u>.</u>

Gaps

0;

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APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Bradgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899.0175.CNUS01
CURRENT APPLICATION NUMBER: US/09/464,099A
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR FILING DATE: 1998-08-20
PRIOR FILING DATE: 1997-04-07
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR FILING DATE: 1991-08-28
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR APPLICATION NUMBER: US 07/576,537
                                                                                                                                                       PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR FILING DATE: 1990-08-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.0
SEQ ID NO 70
LENGTH: 455
TYPE: PRT
TYPE: PRT
ORDINER: Artificial sequence
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                                               Query Match 100.0%; Score 2288; DB 9; Best Local Similarity 100.0%; Pred. No. 7.4e-182; Matches 455; Conservative 0; Mismatches 0;
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
ITITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899-0175.CNUS04 MOSP:175-4
CURRENT APPLICATION NUMBER: US 09/831,696
CURRENT APPLICATION NUMBER: US 09/137,440
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR FILING DATE: 1997-04-07
PRIOR FILING DATE: 1997-04-07
PRIOR FILING DATE: 1991-08-08
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR FILING DATE: 1991-08-28
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR FILING DATE: 1990-08-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                               ; SEQ ID NO 3; LENCTH: 455; TYPE: PRT; ORGANISM: Agrobacterium US-09-861-696-3
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99.8%;
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Pred. No. 2.3e-181;
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APPLICANT: Kishore, Garesh M.
APPLICANT: Kishore, Garesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
CURRENT APPLICATION NUMBER: US/09/464,099A
CURRENT FILING DATE: 1999-12-16
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PRIOR FILING DATE: 1998-08-20
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PRIOR APPLICATION NUMBER: US 08/833,485
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PRIOR FILING DATE: 1990-08-31
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                                                                                                                                                                                                                                         Query Match
Best Local :
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
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                                                                                                                                                                                                                         Matches 454;
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ORGANISM: Agrobacterium
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Pred. No. 2.3e-181;
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 169346
LENGTH: 524
TYPE: PRT
ORGANISM: Glycine max
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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Best Local Similarity
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   VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
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Pred. No. 2.4e-180;
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stallings, William C.
APPLICANT: Stallings, William C.
APPLICANT: Stallings, William C.
TITLE OF INVERTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES FILE REFERENCE: 11899-0175.CNUS04 MOBT:175-4
CURRENT APPLICATION NUMBER: US/09/861,696
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR FILING DATE: 1998-08-20
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR FILING DATE: 1991-08-28
PRIOR FILING DATE: 1991-08-28
PRIOR FILING DATE: 1991-08-31
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR FILING DATE: 1990-08-31
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US-09-861-696-5
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; ORGANISM: Agrobacterium
US-09-861-696-5
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SOFTWARE: PatentIn version 3.0
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VTVDDATMIATSFPEFMDLMAGLGAKIELS
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NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 449
TYPE: PRT
ORGANISM: Pseudomonas sp.
US-09-861-696-7
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US-09-861-696-7
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APPLICANT: Barry, G
APPLICANT: Kishore
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APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
CURRENT FILING DATE: US/09/861,696
CURRENT FILING DATE: US/09/137,440
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR FILING DATE: 1998-08-20
PRIOR FILING DATE: 1998-08-20
PRIOR FILING DATE: 1997-04-07
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR FILING DATE: 1991-08-28
PRIOR FILING DATE: 1991-08-28
PRIOR FILING DATE: 1991-08-28
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373; Conserv
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APPLICANT: PAGGETE, Stephen R.
APPLICANT: Stallings, William C.
FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2

CURRENT APPLICATION NUMBER: US/09/464,099A

CURRENT APPLICATION NUMBER: US 09/137,440

PRIOR APPLICATION NUMBER: US 09/137,440

PRIOR APPLICATION NUMBER: US 09/137,440

PRIOR APPLICATION NUMBER: US 08/833,485

PRIOR FILING DATE: 1997-04-07

PRIOR APPLICATION NUMBER: US 08/833,485

PRIOR PILING DATE: 1997-04-07

PRIOR APPLICATION NUMBER: US 08/306,063

PRIOR APPLICATION NUMBER: US 07/749,611

PRIOR APPLICATION NUMBER: US 07/749,611

PRIOR APPLICATION NUMBER: US 07/749,611

PRIOR FILING DATE: 1991-09-13

PRIOR FILING DATE: 1991-09-28

PRIOR FILING DATE: 1991-08-28

PRIOR FILING DATE: 1990-08-31

NUMBER OF SEQ ID NOS: 70

SEQ ID NO 5

LENGTH: 449

TYDE: DETERMANE: PATCHIAN VERSION 3.0
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    Sequence 7, Application US/09464099A
Patent No. US20020168680A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
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APPLICANT: Kishore,
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ORGANISM: Agrobacterium
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Barry, Gerard r.
Kishore, Ganesh M.
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Sequence 30, Application US/10214766 Publication No. US20030084473A1 GENERAL INFORMATION:

APPLICANT: GoCal, Greg.
TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT
FILE REFERENCE: CA1138
CURRENT APPLICATION NUMBER: US/10/214,766
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,734
PRIOR FILING DATE: 2001-08-09

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RESULT 10
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SEQ ID NO 7
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Best Local
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APPLICANT: Stallings, william C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE:
FILE REFERENCE: 11899.0175.CNUS01 MOST:175-2
CURRENT APPLICATION NUMBER: US/09/464,099A
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR FILING DATE: 1997-04-07
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR FILING DATE: 1994-09-13
PRIOR FILING DATE: 1994-09-13
PRIOR FILING DATE: 1994-09-13
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR FILING DATE: 1994-09-13
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ORGANISM: Pseudomonas
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APPLICATION NUMBER: US 07/576,537
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Pred. No. 1.4e
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
; ORGANISM: Mesorhizobium loti
US-10-369-493-12116
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US-10-369-493-12116
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                               PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12116
LENGTH: 452
TYPE: PRT
                                                                                                                                                                                                                                                                                                                   Sequence 12116, Application US/10369493 Publication No. US20030233675A1
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SOFTWARE: PatentIn version 3.2
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ORGANISM: Brucella melitensis
FEATURE:
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Pred. No. 8.3e-146;
5; Mismatches 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20766
LENGTH: 430
TYPE: PRT
                                                                                                                                              Query Match
Best Local Similarity
Matches 259; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20766, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                     GDASLIKRPMGRVLNPLREMGVQV-KSEDGDRLPVTLRGPKTPTPITYRVPMASAQVKSA 179
KVERTGDCEWRVHGVGVAGFATPEAPLDFGNSGTGCRLAMGAVAGSPIVATFDGDASLRS
                 RIRKEGD-TWIIDGVGNGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDASLTK 127
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                                                                                                                                              Conservative
                                                                                                                                          53.9%; Score 1233.5; DB 15; Length 430;
60.0%; Pred. No. 4.5e-94;
tive 49; Mismatches 113; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 10476
LENGTH: 432
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10476, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                Matches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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                           LVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTV 316
                                                                                                                                                      LREMGVQVKSEDGDRLPVTLRGPKTPTPITYRVPMASAQVKSAVLLAGLNTPGITTVIEP
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                                                                                                                                  LSTMGAEFTASPGGRLPLTLRGISPAVPIEYRLPVASAQVKSAVLLAGLNTPGVTTVIEP
                                                                                                                                                                                                     WHVHGVGVGGLLQPQQALDMGNSGTSTRLLMGLVATHPITATFVGDASLSKRPMGRVIDP
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LVEGSDLVVENVGLNPTRAALFDVLRLMGGSIEELNRREVGGEPVADLRVRHSLLTGIDV
                                                                                   IMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAAL
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Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7814
SEQ ID NO 7814
LENGTH: 418
TYPE: PRT
ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7814
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US-10-369-493-7814
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Best Local Similarity
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                                                                                                                                    PPERAPSMIDEYPILSVVAAFAEGLTIMRGVKELRVKESDRIDAMARGLEACGVRIEEDE
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418
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RESULT 15
US-10-369-493-18039
; Sequence 18039, Application US/10369493
; Publication No. US20030233675A1
; Publication No. US20030233675A1
; GENERAL INFORMATION:
   APPLICANT: Hinkle, Gregory J.
   APPLICANT: Hinkle, Gregory J.
   APPLICANT: Slater, Steven C.
   APPLICANT: Goldman, Barry S.
   APPLICANT: Chen, Xianfeng
   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
   TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
   FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
   PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NOS: 47374
; ORGANISM: SPHINGOMONAS
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Search completed: April 20, 2005, 15:36:19 Job time : 141 secs
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Result
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2005 Compugen
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US-08-476-008-3
US-08-33-485-3
US-09-137-440-3
US-09-137-440-3
US-09-137-440-3
US-08-476-008-5
US-08-476-008-7
US-08-306-063-7
US-08-304-063-7
US-08-833-485-7
US-08-833-485-7
US-09-137-440-5
US-09-137-440-7
US-09-131-151-15
US-09-131-151-15
US-09-137-440-7
US-09-137-440-7
US-09-137-440-7
US-09-137-440-7
US-09-137-440-7
US-09-137-440-67
US-09-137-433-4297
US-09-107-333-4297
US-09-107-333-7163
US-09-107-333-4297
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US-08-306-063-44	US-08-476-008-44	US-09-134-001C-3223	US-09-325-881-4	US-09-226-091-4	US-08-896-345-4	US-09-134-000C-4980	US-09-137-440-42	US-08-833-485-42	US-08-306-063-42	US-08-476-008-42	US-09-226-091-2	US-08-896-345-2	US-09-325-881-2	US-09-583-110-3546	US-09-137-440-69	US-08-833-485-69	US-08-306-063-69
Sequence 44, Appl	Sequence 44, Appl	Sequence 3223, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4980, Ap	Sequence 42, Appl	Sequence 42, Appl	Sequence 42, Appl	Sequence 42, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 3546, Ap	Sequence 69, Appl	Sequence 69, Appl	Sequence 69, Appl

## ALIGNMENTS

NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914 REFERENCE/DOCKET NUMBER: 38-21(10660)A TELECOMMUNICATION INFORMATION: TELEPHONE: (314)537-6099 TELEFAX: (314)537-6047 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 455 amino acids TYPE: amino acid TOPOLOGY: linear	APPLICATION NUMBER: US/08/476,008 FILING DATE: 07-JUN-1995 CLASSIFICATION 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/306,063 FILING DATE: 13-SEP-1994 APPLICATION NUMBER: US 07/749,611 FILING DATE: 28-AUG-1991 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/576,537 FILING DATE: 31-AUG-1990 CLASSIFICATION: 435 CLASSIFICATION: 435 PRIOR APPLICATION ADTA: APPLICATION NUMBER: US 07/576,537 FILING DATE: 31-AUG-1990 CLASSIFICATION: 435	oerner, Jr., Monsanto Co. ld Village Parkway	ຫຼຸດຮູ <del>ເ</del>
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Best Local Similarity
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
FILING DATE: 28-AUG-1991 CLASSIFICATION: 435 RIOR APPLICATION DATA:
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Pred. No. 1.9e-
0; Mismatches
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-306-063-3
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Patent No. 5804425
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (314)537-6047 INFORMATION FOR SEQ ID NO: 3:
                                                                                             APPLICANT: Barry, Gerard F.

APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.

TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
STATE: N
COUNTRY:
                                 CITY: St.
                                                   STREET:
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                 Missouri
                                                 E: Dennis R. Hoerner, Jr., Monsa
700 Chesterfield Village Parkway
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Pred. No. 1.9e-201;
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FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
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NAME: HOERNEY Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
US 08/306,063
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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)GY: linear
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                                VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455
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(314)737-6047
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Pred. No. 1.9e-201;
0; Mismatches 1;
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Best Local (
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/
FILING DATE: 31-AUG-1990
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MEDLUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
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REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 07-APR-
APPLICATION NUMBER:
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STATE: Min
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                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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Rishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.
TNVENTION: Glyphosate Tolerant
LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
                                                                           GDASLTKRPMGRVLNPLREMGVQVKSEDGDRLPVTLRGPKTPTPITYRVPMASAQVKSAV 180
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Pred. No. 1.9e-201;
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Best Local S
Matches 454
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                                                                                                                                                                                                                                                                                                 NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESSE: Dennis R. Hoerner, Jr., Monsanto Co.
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co.
STREET: 700 Chesterfield Village Parkway
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TYPE: A
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FILING DATE: 19910828
CLASSIFICATION: 800
                                                                                             Local Similarity
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                       MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
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 VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455
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                                                                                                                                                                                                                                                                                     (314)537-6047
                                                                           Conservative
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SYSTEM: PC-DOS/MS-DOS
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99.8%;
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                                                                           Score 2282; DB 5;
Pred. No. 1.9e-201;
0; Mismatches 1;
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                                                                                                            Length 455;
                                                                           Indels
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APPLICANT: Barry, Gerard F.

APPLICANT: Kishore, Ganesh M.

APPLICANT: Padgette, Stephen R.

APPLICANT: Stallings, William C.

APPLICANT: Stallings, William C.
                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOETNET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 31-AUG-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 28-AUG-1991 CLASSIFICATION: 435
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STREET: 7
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RESULT 7
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; Sequence 7, Application US/08476008
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Best Local Similarity
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Barry, Gerard F.

APPLICANT: Kishore, Ganesh i

APPLICANT: Padgette, Stephe
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TELEPAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                    NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsar
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate
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                                                                                                                                                        STREET: 70
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TOPOLOGY: linear
                                                                                                                                            STATE:
APPLICATION NUMBER:
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US/08/476,008
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Pred. No. 2.4e-166;
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Sequence 5, Application Patent No. 5633435
GENERAL INFORMATION:

Application US/08306063

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Barry, Gerard F. Kishore, Ganesh M. Padgette, Stephen R. Stallings, William C.

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RESULT 8
US-08-306-063-5
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SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
TOPOLCGY: linear
MOLECULE TYPE: protein
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Best Local 9
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
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APPLICATION NUMBER: U
FILING DATE: 31-AUG-1
CLASSIFICATION: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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73; Conservative
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82.9%; Pred. No. 2.46
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; MOLECULE TYPE: protein US-08-306-063-5
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Best Local Similarity
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/306,063
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APPLICATION NUMBER: 1
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REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
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CLASSIFICATION: 435
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VARGLEANGVDCTEGEMSLTVRGRPDGKGLG
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Pred. No. 2.4
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Best Local (
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 1
FILING DATE: 28-AUG-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co.
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
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CLASSIFICATION:
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STATE: Missouri
                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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IBM PC compatible
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                                                                                                                                                                                        32; Mismatches
                                                                                                                                                                                                       Score 1900.5; DB 1;
Pred. No. 2.4e-166;
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                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HOERNER Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co.
STREET: 700 Chesterfield Village Parkway
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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 28-AUG-1991 CLASSIFICATION: 435
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STATE: Missouri
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RESULT 11
US-08-833-485-7
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Matches
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                                        SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/833,485
FILING DATE: 07-APR-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
PRIOR APPLICATION DATA
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             FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                                     CITY: St. Louis
STATE: Missouri
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700 Chesterfield Village Parkway
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Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.
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82.9%; Pred. No. 2.4e
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RESULT 12
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                                                                                                                                     Sequence 5, Application US/09137440
Patent No. 6248876
GENERAL INFORMATION:
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Best Local Similarity
Matches 373; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
                                          APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                 NUMBER OF SEQUENCES:
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                 CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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    ADDRESSEE:
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   R. Hoerner,
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Pred. No. 2.4e-
32; Mismatches
Jr.,
   Monsanto Co.
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REGISTRATION NUMBER: 30,914
REFERENCE DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6049
TELEPAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Matches 373;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 07-APR-
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TOPOLOGY:
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OPERATING SYSTEM:
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FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
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VTVDDATMIATSFPEFMDLMAGLGAKIELS
                                                             VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
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                                     VARGLEANGVDCTEGEMSLTVRGRPDGKGLG----GGTVATHLDHRIAMSFLVMGLAAEKP
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82.9%; Pred. No. 2.4e-166;
tive 32; Mismatches 42;
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US-09-137-440-7
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Best Local
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APPLICATION NUMBER: US 0'
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
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TYPE: a
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FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                        RAMQAMGAKIRKEGDVWIINGVGNGCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI
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amino acid
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GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMASAQVKSAV
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                                                                                                                                                                                                                                          83.1%; Score 1900.5;
82.9%; Pred. No. 2.46
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Query Match 83.1%; Score 1900.5; Best Local Similarity 82.9%; Pred. No. 2.44 Matches 373; Conservative 32; Mismatches
                                                                                                                                                            TELEPHONE: (314)537-609
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19910828
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSES: Dennis R. Hoerner, Jr., Monsanto Co.
STREET: 700 Chesterfield Village Parkway
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APPLICANT: Padgette, Stephen R.

TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                            FILING DATE: 31-AUG-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                         TYPE: AMI
                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: St. Louis
STATE: Missouri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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PCT-US91-06148A-7
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             FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOERNEY JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
                                                                                                                                                         APPLICATION NUMBER: PCT/US91/06148A
FILING DATE: 19910828
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US 07/576,537
APPLICATION NUMBER: US 07/576,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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STREET: 700 Chesterfield Village Parkway
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Y: USA
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; SEQUENCE CHARACTERISTICS:
; LENCTH: 449 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
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VTVDDSNMIATSFPEFMDMMPGLGAKIELS
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82.9%; Pred. No. 2.40
tive 32; Mismatches
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Search completed: April 20, 2005, 15:24:34
Job time : 51 secs